

CLAIMS

1. A method for obtaining transgenic plants having an increased capacity to synthesize, to accumulate and to exude organic acids, by integration into their genome of a recombinant heterologous DNA molecule encoding enzymes that synthesize organic acids, involving the following steps:

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- (a) preparation of a recombinant heterologous DNA molecule encoding one or more genes for enzymes that synthesize organic acids, linked to a promoter sequence functional in plants, and to a transcription termination/polyadenylation sequence functional in plants;
  - (b) the transformation of plant cells with the recombinant DNA molecule, and
  - (c) the regeneration of transgenic plants starting from transformed cells, or of seeds from plants obtained from these transformed cells, for one or several generations, wherein the genetic information of these transformed cells, includes the ~~recombinant DNA molecule coding for enzymes that synthesize organic acids.~~

2. The method according to claim 1, in which the recombinant DNA molecule comprises one or more microbial genes coding for enzymes that synthesize organic acids.

3. The method according to claim 1, wherein the recombinant DNA molecule comprises a gene of plant origin coding for an enzyme that synthesizes organic acids.

4. The method according to claim 1, wherein the recombinant DNA molecule comprises a gene of animal origin coding for an enzyme that synthesizes organic acids.

5. The method according to claim 2, wherein the recombinant DNA molecule comprises one or more bacterial genes that code for an enzyme that synthesizes organic acids.

6. The method according to claim 1, wherein the recombinant molecule comprises a gene that codes for the enzyme Citrate Synthase.

7. The method according to claim 1, wherein the recombinant molecule comprises a gene that codes for the enzyme Malate dehydrogenase.

8. The method according to claim 1, wherein the enzyme that synthesizes organic acids is located in the cytoplasm.

9. The method according to claim 1, wherein the enzyme that synthesizes organic acids is located in chloroplasts.

10. The method according to claim 1, wherein the enzyme that synthesizes organic acids is located in the mitochondria.

11. The method according to claim 5, wherein the recombinant molecule comprises a gene of *Pseudomonas aeruginosa* that codes for Citrate Synthase.

12. The method according to claim 1, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

13. The method according to claim 2, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

14. The method according to claim 3, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

15. The method according to claim 4, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

16. The method according to claim 5, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

17. The method according to claim 6, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

18. The method according to claim 7, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

19. The method according to claim 8, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

20. The method according to claim 9, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.

21. The method according to claim 10, wherein the transcription termination sequence is the transcription termination sequence of the Nopaline Synthetase gene.
22. The method according to claim 1, wherein the promoter is a constitutive promoter.
23. The method according to claim 2, wherein the promoter is a constitutive promoter.
24. The method according to claim 3, wherein the promoter is a constitutive promoter.
25. The method according to claim 4, wherein the promoter is a constitutive promoter.
26. The method according to claim 5, wherein the promoter is a constitutive promoter.
27. The method according to claim 6, wherein the promoter is a constitutive promoter.
28. The method according to claim 7, wherein the promoter is a constitutive promoter.
29. The method according to claim 8, wherein the promoter is a constitutive promoter.
30. The method according to claim 9, wherein the promoter is a constitutive promoter.
31. The method according to claim 10, wherein the promoter is a constitutive promoter.

32. The method according to claim 1, wherein the promoter is a root-specific promoter.
33. The method according to claim 2, wherein the promoter is a root-specific promoter.
34. The method according to claim 3, wherein the promoter is a root-specific promoter.
35. The method according to claim 4, wherein the promoter is a root-specific promoter.
36. The method according to claim 5, wherein the promoter is a root-specific promoter.
37. The method according to claim 6, wherein the promoter is a root-specific promoter.
38. The method according to claim 7, wherein the promoter is a root-specific promoter.
39. The method according to claim 8, wherein the promoter is a root-specific promoter.
40. The method according to claim 9, wherein the promoter is a root-specific promoter.
41. The method according to claim 10, wherein the promoter is a root-specific promoter.
42. The method according to claim 1, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

43. The method according to claim 2, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

44. The method according to claim 3, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

45. The method according to claim 4, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

46. The method according to claim 5, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

47. The method according to claim 6, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

48. The method according to claim 7, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

49. The method according to claim 8, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

50. The method according to claim 9, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

51. The method according to claim 10, wherein the promoter is a promoter inducible by stress caused by low Phosphate availability.

52. The method according to claim 1, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

53. The method according to claim 2, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

54. The method according to claim 3, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

55. The method according to claim 4, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

56. The method according to claim 5, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

57. The method according to claim 6, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

58. The method according to claim 7, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

59. The method according to claim 8, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

60. The method according to claim 9, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

61. The method according to claim 10, wherein the promoter is a promoter inducible by stress caused by low Iron availability.

62. The method according to claim 1, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

63. The method according to claim 2, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

64. The method according to claim 3, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

65. The method according to claim 4, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

66. The method according to claim 5, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

67. The method according to claim 6, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

68. The method according to claim 7, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

69. The method according to claim 8, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

70. The method according to claim 9, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

71. The method according to claim 10, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

72. The method according to claim 9, wherein the recombinant molecule comprises a signal peptide sequence to direct a heterologous enzyme that synthesizes organic acids to the chloroplast or the mitochondria of the transgenic cells.

73. The method according to claim 10, wherein the recombinant molecule comprises a signal peptide sequence to direct a heterologous enzyme that synthesizes organic acids to the chloroplast or the mitochondria of the transgenic cells.

74. A recombinant heterologous DNA molecule comprising one or more genes that code for enzymes that synthesize organic acids, functionally linked to a promoter sequence functional in plants, and to a transcription termination/polyadenylation sequence functional in plants.

75. The recombinant DNA molecule according to claim 74, wherein the coding sequence for the enzyme that synthesizes organic acids, is from one or more microbial genes.

76. The recombinant DNA molecule according to claim 74, wherein the coding sequence for the enzyme that synthesizes organic acids is from a gene of plant origin.

77. The recombinant DNA molecule according to claim 74, wherein the coding sequence for the enzyme that synthesizes organic acids is from a gene of animal origin.

78. The recombinant DNA molecule according to claim 74, wherein the coding sequence for the enzyme that synthesizes organic acids, is from one or more bacterial genes.

79. The recombinant DNA molecule according to claim 74, wherein the gene that codes for the enzyme that synthesizes organic acids is a gene that codes for the enzyme citrate synthase.

80. The recombinant DNA molecule according to claim 74, wherein the gene that codes for the enzyme that synthesizes organic acids is a gene of *Pseudomonas aeruginosa* that codes for the enzyme citrate synthase.

81. The recombinant DNA molecule according to claim 74, wherein the gene that codes for the enzyme that synthesizes organic acids is a gene that codes for the enzyme Malate dehydrogenase.

82. The recombinant DNA molecule according to claim 74, wherein the gene that codes for the enzyme that synthesizes organic acids is an enzyme that is located in the cytoplasm.

83. The recombinant DNA molecule according to claim 74, wherein the gene that codes for the enzyme that synthesizes organic acids is an enzyme that is located in the chloroplast.



84. The recombinant DNA molecule according to claim 74, wherein the promoter is a constitutive promoter.

85. The recombinant DNA molecule according to claim 74, wherein the promoter is a root-specific promoter.

86. The recombinant DNA molecule according to claim 74, wherein the promoter is a promoter whose expression is inducible by stress caused by low phosphate availability.

87. The recombinant DNA molecule according to claim 74, wherein the promoter is a promoter whose expression is inducible by stress caused by low iron availability.

88. The recombinant DNA molecule according to claim 74, wherein the promoter is the 35S promoter of the cauliflower mosaic virus.

89. The recombinant DNA molecule according to claim 74 comprising a sequence that includes a transit peptide sequence for chloroplast or mitochondrial protein targeting in plants.

90. The recombinant DNA molecule according to claim 74, comprising a transcription termination/polyadenylation sequence that is the transcription termination/polyadenylation sequence of the Nopaline Synthetase gene.

91. The recombinant DNA molecule according to claim 74, as defined in figure 1.

~~92. The vector comprising the recombinant DNA molecule according to claim 74.~~

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93. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 74.

94. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 75.

95. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 76.

96. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 77.

97. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 78.

98. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 79.

99. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 80.

100. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 81.

101. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 82.

102. Transgenic plants with increased capacity to synthesize, to accumulate and to exude organic acids by integration into their genome of a recombinant heterologous DNA molecule as defined in claim 83.

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~~111.~~ Transgenic plants according to claim 93, tolerant to toxic concentrations of Aluminum.

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~~112.~~ Transgenic plants according to claim 93, having increased capacity to solubilize or accumulate phosphate.

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~~113.~~ Transgenic plants according to claim 93, having increased capacity to solubilize or accumulate iron.

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~~114.~~ Transgenic plants according to claim 93, requiring less fertilizer for their growth.

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~~115.~~ Transgenic plants according to claim 93, that develop better or have higher productivity in acid soils.

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~~116.~~ The transgenic plants according to claim 93, wherein the plant is a monocotyledonous plant.

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~~117.~~ Transgenic plants according to claim 93, wherein the plant is a dicotyledonous plant.

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~~118.~~ Transgenic plants according to claim ~~115~~ <sup>107</sup>, wherein the plant belongs to anyone of the families: Poaceae or Lileaceae.

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~~119.~~ Transgenic plants according to claim ~~117~~ <sup>109</sup>, wherein the plant belongs to anyone of the families: Leguminoseae, Solanaceae, Caricaceae or Cucurbitaceae.

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~~120.~~ Transgenic plants according to claim ~~116~~ <sup>108</sup>, wherein the plant belongs to any of the species: Triticum spp, Oryza sativa, Zea mays, Sorghum bicolor, Avena sativa or Saccharum officianarum.

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~~121.~~ Transgenic plants according to claim ~~117~~ <sup>109</sup>, wherein the plant belongs to any of the species: Solanum tuberosum, Lycopersicum esculentum or Glycine max.

~~114~~ 122. Transgenic plants according to claim ~~117~~<sup>109</sup>, wherein the plant is of the Nicotiana genus.

~~115~~ 123. Transgenic plants according to claim ~~122~~<sup>114</sup>, wherein the plant is of the Nicotiana tabacum species.

~~116~~ 124. Transgenic plants according to claim ~~117~~<sup>109</sup>, wherein the plant is of the Carica genus.

~~117~~ 125. Transgenic plants according to claim ~~124~~<sup>116</sup>, wherein the plant is of the Carica papaya species.

~~118~~ 126. Use of the transgenic plants according to claim 81 in acid soils.

~~119~~ 127. Use of the transgenic plants according to claim 81 in soils containing phosphates in forms not available for the plant nutrition.

~~120~~ 128. Use of the transgenic plants according to claim 81, for practice or cultivation systems that use less fertilizer.

~~121~~ 129. The transgenic seeds or any vegetative reproductive structure attainable from a transgenic plant as defined in the claim 81.

~~122~~ 130. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 74.

~~123~~ 131. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 75.

~~124~~ 132. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 76.

~~125~~ 133. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 77.

~~126~~

134. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 78.

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135. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 79.

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136. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 80.

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137. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 81.

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138. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 82.

~~131~~

139. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 83.

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140. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 81.

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141. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 85.

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142. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 86.

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143. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 87.

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144. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 88.

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145. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 89.

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146. A transformed cell or protoplast transformed with the recombinant DNA molecule as defined in claim 90.